

The invention provides a cell composition comprising a population of non-yeast eukaryotic cells containing a diverse population of variant nucleic acids, each of the variant nucleic acids being expressed in a different cell and located within each cell at an identical site in the genome. The invention also provides a method of identifying a polypeptide exhibiting optimized activity by screening a population of non-yeast eukaryotic cells containing a diverse population of variant nucleic acids for an activity associated with a parent polypeptide of a diverse population of variant polypeptides encoded by the variant nucleic acids; and identifying a variant polypeptide exhibiting an optimized activity relative to the parent polypeptide.